SEQUENCE LISTING

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<120> MYROTHECIUM SP. TRANSFORMATION AND EXPRESSION SYSTEM

<130> VANM260.001APC

<140> US 10/525,984
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<151> 2002-o8-2002

<160> 37

<170> PatentIn version 3.2

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<210> 7
<211> 1052
<212> DNA
<213> Myrothecium

<220>

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cccggcccga gttgtaattt gcagaggatg cttttggcga ggtgccttcc gagttccctg 120
gaacgggacg ccatagaggg tgagagcccc gtctggtcgg acaccgagcc tctgtaaagc 180
tccttcgacg agtcgagtag tttgggaatg ctgctcaaaa tgggaggtat atgtcttcta 240
aagctaaata ttggccagag accgatagcg cacaagtaga gtgatcgaaa gatgaaaagc 300
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<211> 1040
<212> DNA
<213> Myrothecium

<220>

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<223> 28s rDNA sequence of the strain MUCL11831

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ctttggaaag agagttaaac agcacgtgaa attgttaaaa gggaagcgtt tacgaccaga 360
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cagttcgccg cgggggataa aggcgtcggg aatgtggctc ccccgggagt gttatagccc 480
ttcgcgcaat accctgaggc ggactgaggt tcgcgcattc gcaaggatgc tggcgtaatg 540
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<211> 1012
<212> DNA
<213> Myrothecium

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<223> 28s rDNA sequence of the strain CBS449.71

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aacgggacgc catagagggt gagagccccg tctggtcgga caccgagcct ctgtaaagct 180
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ctttgaaaag agagttaaat agcacgtgaa attgttgaaa gggaagcgtt tatgaccaga 360
cttggcccgg ttgatcatcc agccttctgg ctggtgcact ctgccggtcc aggccagcat 420
cagttcgtcg cgggggataa aggtttcggg aatgtagctc ctccgggagt gttatagccc 480
gttgcgtaat accctgcggt ggactgaggt ccgcgctctg caaggatgct ggcgtaatgg 540
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gtgtaaaacc cctacgcgta atgaaagtga acgcaggtga gagcttcggc gcatcatcga 660
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ggtaaagcga atgattaggg actcgggggc gctatttagc cttcatccat tctcaaactt 960

taaatatgta agaagccctt gttgcttaat tgaacgtggg cattcgaatg ta 1012

<210> 10
<211> 1038
<212> DNA
<213> Myrothecium

<220>

<221> misc_feature
<223> 28s rDNA sequence of the strain IMI140595

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taggcccgag ttgtaatttg cagaggatgc ttttggcgag gtgccttccg agttccctgg 120
aacgggacgc catagagggt gagagccccg tctggtcgga caccgagcct ctgtaaagct 180
ccttcgacga gtcgagtagt ttgggaatgc tgctcaaaat gggaggtata tgtcttctaa 240
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cagttcgccg cgggggataa aggtttcggg aatgtggctc ctccgggagt gttatagccc 480
gttgcgtaat accctgcggt ggactgaggt ccgcgcttct gcaaggatgc tggcgtaatg 540
gtcatcaacg acccgtcttg aaacacggac caaggagtcg tcttcgtatg cgagtgttcg 600
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accgatcctg atgttctcgg atggatttga gtaagagcat acggggccgg acccgaaaga 720
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tagtgggcca tttttggt 1038

<210> 11
<211> 1044
<212> DNA
<213> Myrothecium

<220>

<221> misc_feature
<223> 28s rDNA sequence of the strain IMI29040

<400> 11

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cccggcccga gttgtaattt gcagaggatg cttttggcaa ggtgccttcc gagttccctg 120
gaacgggacg ccatagaggg tgagagcccc gtctggtcgg acaccgagcc tctgtaaagc 180
tccttcgacg agtcgagtag tttgggaatg ctgctcaaaa tgggaggtat atgtcttcta 240
aagctaaata ccggccagag accgatagcg cacaagtaga gtgatcgaaa gatgaaaagc 300
actttgaaaa gagagttaaa tagcacgtga aattgttgaa agggaagcgt ttatgaccag 360
acttggcccg gttgatcatc cagcgttctc gctggtgcac tctgccggtc caggccagca 420
tcagttcgtc gcgggggata aaggcttcgg gaatgtagct ctcttcgggg agtgttatag 480
cccgttgtgt aataccctgc ggtggactga ggtccgcgct ctgcaaggat gctggcgtaa 540
tggtcatcac gaccgtcttg aaacacggac caaggagtcg tcttcgtatg cgagtgttcg 600
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ttaaatatgt aagaagccct tgttgcttaa ttgaacgtgg gcattcgaat gtatcaacac 1020
tagtgggcca tttttggtaa gcag 1044

<210> 12
<211> 445
<212> DNA
<213> Myrothecium

<220>
<221> misc_feature
<223> ITS sequence of the strain MUCL39210

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aacggatctc ttggttctgg catcgatgaa gaacgcagcg aaatgcgata agtaatgtga 180
attgcagaat tcagtgaatc atcgaatctt tgaacgcaca ttgcgccccgc cagtattctg 240
gcgggcatgc ctgttcgagc gtcatttcaa ccctcaggcc cccagtgcct ggcgttgggg 300
atcggcacca gggcgtccgc gcaagcggtc tccccgccgg ccccgaaatc tagtggcggt 360
ctcgctgtag tcctcctctg cgtagtagca caacctcgca gctggaactc ggcggtggcc 420
ctgccgttaa acaccccact tctga 445

<210> 13
<211> 459
<212> DNA
<213> Myrothecium

<220>
<221> misc_feature
<223> ITS sequence of the strain MUCL11831

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actcaatgtt tttcatgcag tattatctga gtggcaaacg caaaaaataa atcaaaactt 120
ttaacaacgg atctcttggc tctggcatcg atgaagaacg cagcgaaatg cgataagtaa 180
tgtgaattgc agaattcagt gaatcatcga atctttgaac gcacattgcg cccgcgagta 240
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cgcggcgctg gtgttgggga tcggccctaa accgccgtcc cccaaattca gtggcggtct 360
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gtaaaacccc cgactttctg aacgttgacc tcggatcag 459

<210> 14
<211> 423
<212> DNA
<213> Myrothecium

<220>
<221> misc_feature
<223> ITS sequence of the strain CBS449.71

<400> 14

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acaacggatc tcttggttct ggcatcgatg aagaacgcag cgaaatgcga taagtaatgt 180
gaattgcaga attcagtgaa tcatcgaatc tttgaacgca cattgcgccc gccagtattc 240
tggcgggcat gcctgttcga gcgtcatttc aaccctcagg cccccagtgc ctggtgttgg 300
ggatcggccc agccttctcg caaggccgcc ggccccgaaa tctagtggcg gtctcgctgt 360
agtcctcctc tgcgtagtag cacaacctcg cagttggaac gcggcggtgg ccatgccgtt 420
aaa 423

<210> 15
<211> 445
<212> DNA

<213> Myrothecium

<220>
<221> misc_feature
<223> ITS sequence of the strain IMI140595

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ctatgtttta ctgtacatct cctctgagtg acacataaac aataaataaa aactttcaac 120
aacggatctc ttggttctgg catcgatgaa gaacgcagcg aaatgcgata agtaatgtga 180
attgcagaat tcagtgaatc atcgaatctt tgaacgcaca ttgcgccccgc cagtattctg 240
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ccctgccgta aaacacccca cttct 445

<210> 16
<211> 434
<212> DNA
<213> Myrothecium

<220>
<221> misc_feature
<223> ITS sequence of the strain IMI290405

<400> 16

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acaacggatc tcttggttct ggcatcgatg aagaacgcag cgaaatgcga taagtaatgt 180
gaattgcaga attcagtgaa tcatcgaatc tttgaacgca cattgcgccc gccagtattc 240
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acaccccact tctg 434

<210> 17
<211> 24
<212> DNA
<213> Artificial

<220>
<223> AMY1 primer

<400> 17

ggaattccac agaaggcatt tatg 24

<210> 18
<211> 23
<212> DNA
<213> Artificial

<220>
<223> AMY2 primer

<400> 18

gctctagagc aaccaccagg tca 23

<210> 19
<211> 17

<212> DNA
<213> Artificial

<220>
<223> Gpd1 primer

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<223> n is A, C, T or G

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is dInosine

<400> 19
ggnatcaayg gnttcgg 17

<210> 20
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Gpd2 primer

<400> 20

gtgswgswgg ggatgatgtt 20

<210> 21
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Gpd3 primer

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is A, C, T or G

<220>
<221> misc_feature
<222> (18)..(18)
<223> n is dInosine

<400> 21

ggtcgtatcg tnttycgnaa ygc 23

<210> 22
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Gpd4 primer

<220>
<221> misc_feature

<222> (18)..(18)
<223> n is dInosine

<400> 22
ggagccaggc agttggtngt rca 23

<210> 23
<211> 836
<212> DNA
<213> Myrothecium

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<221> misc_feature
<223> gpd gene sequence of the strain MUCL11831

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atgatggtgt acttgtcgtt gaggaccttg gcgaggggag ccaggcagtt ggtggtgcac 180
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ccgttgacgc tcaggtcagc gccatcggcc tcgacctcac ccttgaagag accgtgggtg 480
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aagaaagcag atgtcaaggt tggcgggaaa agacgatgga ggggcacggg tttggacatg 600
gttgcaggta ggtggggtgc aacggcccat gtcattgcaa gcatgccatg tcgggttttg 660
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<210> 24
<211> 954
<212> DNA
<213> Myrothecium

<220>
<221> misc_feature
<223> gpd gene sequence of the strain CBS449.71

<400> 24

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tgatggtgaa cttgtcgtgg atgaccttgg cgaggggagc caggcagttg gtggtgcaag 180
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<210> 25
<211> 1055
<212> DNA

<213> Myrothecium

<220>
<221> misc_feature
<223> gpd gene sequence of the strain IMI290405

<400> 25

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atgatggtga acttgtcgtg aatgaccttg gcgagaggag ccaggcagtt ggtggtgcag 180
gaggcgttgg agatgacgtc ggcgctgccg tcgtaggtct cctcgttgac acccataacg 240
tacatgggag catcagcaga gggggcagag atgatgacct tcttggcacc acccttcaag 300
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ccgttgacgg tcaggtcagc gccatcgacg gtgacctcac ccttgaagac gccgtgggtg 480
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acgatacgac caatgcggcc gaacccattg atacc 1055

<210> 26
<211> 850
<212> DNA
<213> Myrothecium

<220>
<221> misc_feature
<223> gpd gene sequence of Myrothecium gramineum (Xepiculopis graminea) MUCL39210

<400> 26

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tacgctgtaa gtgctgcttc tgcttccct cagtcgacga gcgagcccaa agccgagctg 120
cagctagcgg agccatgcgc tgcctgcatg ccactgcata acagcagcta gaggaggggt 180
acacggccgc gcgcgcagac acacatacaa caccaccacc accaaaagga ggggcagaaa 240
aaatccagca ttgtccgatt tcaccccacc atctcacgtc aaccaatttg cccctccatg 300
atatcatgtg tccgcgccca gctcaacacg tccacctcct ctggccaatg gcgagcgcat 360
tgatgctttg atgagcggaa acgacgctga ggccctcagc ctcgtcgtcg ctgccgctgc 420
cgccgcgcgc cgctcacgca tcggcgggct cccgtcgctg ggcttcaatt gacatgacat 480
gatgcatggc caccgtgcta accacccctg tgtctgtccg ataggcctac atgctcaagt 540
atgactctac ccacggtctc ttcaagggtg aggtcaccgt cgatggcgat gacctgaccg 600
tcaacggcaa gaaggtccgc ttctacactg agcgtgaccc cgccgccatc ccctggaagg 660
agactggtgc cgagtacatt gtcgagtcca ccggtgtctt caccaccaag gacaaggctg 720
ctgctcacct gaagggtggt gccaagaagg tcatcatctc tgccccctct gccgatgccc 780
ccatgtacgt tatgggtgtc aacgaggaga cctacgacgg cagcgccgac gtcatctcca 840
acgcttcttg 850

<210> 27
<211> 130
<212> PRT
<213> Myrothecium

<220>
<221> MISC_FEATURE
<223> glyceraldehyde 3-P dehydrogenase sequence of Myrothecium

gramineum (Xepiculopis graminea) MUCL39210

<400> 27
Ala Val Glu His Ser Asp Val Glu Ile Val Ala Val Asn Asp Pro Phe
1 5 10 15
Ile Glu Pro Lys Tyr Ala Ala Tyr Met Leu Lys Tyr Asp Ser Thr His
20 25 30
Gly Leu Phe Lys Gly Glu Val Thr Val Asp Gly Asp Asp Leu Thr Val
35 40 45
Asn Gly Lys Lys Val Arg Phe Tyr Thr Glu Arg Asp Pro Ala Ala Ile
50 55 60
Pro Trp Lys Glu Thr Gly Ala Glu Tyr Ile Val Glu Ser Thr Gly Val
65 70 75 80
Phe Thr Thr Lys Asp Lys Ala Ala Ala His Leu Lys Gly Gly Ala Lys
85 90 95
Lys Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met Tyr Val Met
100 105 110
Gly Val Asn Glu Glu Thr Tyr Asp Gly Ser Ala Asp Val Ile Ser Asn
115 120 125
Ala Ser
130

<210> 28
<211> 21
<212> DNA
<213> Artificial

<220>
<223> hphpCSN431 primer

<400> 28

atgcctgaac tcaccgcgac g 21

<210> 29
<211> 18
<212> DNA
<213> Artificial

<220>
<223> hphpCSN432 primer

<400> 29

ctattccttt gccctcgg 18

<210> 30
<211> 16
<212> DNA
<213> Artificial

<220>
<223> GPD2 primer

<400> 30

tctggcatgc ggagag 16

<210> 31
<211> 16
<212> DNA
<213> Artificial

<220>
<223> AMY5 primer

<400> 31
cgatgatgcc ctgcca 16

<210> 32
<211> 850
<212> DNA
<213> Myrothecium

<220>
<221> CDS
<222> (1)..(66)

<220>
<221> misc_feature
<222> (1)..(850)
<223> partial nucleotide sequence and its deduced protein sequence of the Myrothecium gramineum MUCL39210 glyceraldehyde-3-P dehydrogenase gene

<220>
<221> CDS
<222> (525)..(848)

<400> 32

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1               5                  10                  15
att gag ccc aag tac gct gtaagtgctg cttctgcttc ccctcagtcg              96
Ile Glu Pro Lys Tyr Ala
            20
acgagcgagc ccaaagccga gctgcagcta gcggagccat gcgctgcctg catgccactg     156
cataacagca gctagaggag gggtacacgg ccgcgcgcgc agacacacat acaacaccac     216
caccaccaaa aggaggggca gaaaaaatcc agcattgtcc gatttcaccc caccatctca     276
cgtcaaccaa tttgcccctc catgatatca tgtgtccgcg cccagctcaa cacgtccacc     336
tcctctggcc aatggcgagc gcattgatgc tttgatgagc ggaaacgacg ctgaggccct     396
cagcctcgtc gtcgctgccg ctgccgccgc gcgccgctca cgcatcggcg ggctcccgtc     456
gctgggcttc aattgacatg acatgatgca tggccaccgt gctaaccacc cctgtgtctg     516
tccgatag gcc tac atg ctc aag tat gac tct acc cac ggt ctc ttc aag      566
        Ala Tyr Met Leu Lys Tyr Asp Ser Thr His Gly Leu Phe Lys
                25                  30                  35
ggt gag gtc acc gtc gat ggc gat gac ctg acc gtc aac ggc aag aag       614
Gly Glu Val Thr Val Asp Gly Asp Asp Leu Thr Val Asn Gly Lys Lys
            40                  45                  50
gtc cgc ttc tac act gag cgt gac ccc gcc gcc atc ccc tgg aag gag       662
Val Arg Phe Tyr Thr Glu Arg Asp Pro Ala Ala Ile Pro Trp Lys Glu
        55                  60                  65
act ggt gcc gag tac att gtc gag tcc acc ggt gtc ttc acc acc aag       710
Thr Gly Ala Glu Tyr Ile Val Glu Ser Thr Gly Val Phe Thr Thr Lys
    70                  75                  80
gac aag gct gct gct cac ctg aag ggt ggt gcc aag aag gtc atc atc       758
Asp Lys Ala Ala Ala His Leu Lys Gly Gly Ala Lys Lys Val Ile Ile
85                  90                  95                  100
tct gcc ccc tct gcc gat gcc ccc atg tac gtt atg ggt gtc aac gag       806
Ser Ala Pro Ser Ala Asp Ala Pro Met Tyr Val Met Gly Val Asn Glu
                105                 110                 115
gag acc tac gac ggc agc gcc gac gtc atc tcc aac gct tct tg           850
Glu Thr Tyr Asp Gly Ser Ala Asp Val Ile Ser Asn Ala Ser
            120                 125                 130
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<210> 33
<211> 22
<212> PRT
<213> Myrothecium

<400> 33

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Ala Val Glu His Ser Asp Val Glu Ile Val Ala Val Asn Asp Pro Phe
1               5                  10                  15
Ile Glu Pro Lys Tyr Ala
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<210> 34
<211> 108
<212> PRT
<213> Myrothecium

<400> 34

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Ala Tyr Met Leu Lys Tyr Asp Ser Thr His Gly Leu Phe Lys Gly Glu
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Val Thr Val Asp Gly Asp Asp Leu Thr Val Asn Gly Lys Lys Val Arg
            20                  25                  30
Phe Tyr Thr Glu Arg Asp Pro Ala Ala Ile Pro Trp Lys Glu Thr Gly
        35                  40                  45
Ala Glu Tyr Ile Val Glu Ser Thr Gly Val Phe Thr Thr Lys Asp Lys
    50                  55                  60
Ala Ala Ala His Leu Lys Gly Gly Ala Lys Lys Val Ile Ile Ser Ala
65                  70                  75                  80
Pro Ser Ala Asp Ala Pro Met Tyr Val Met Gly Val Asn Glu Glu Thr
                85                  90                  95
Tyr Asp Gly Ser Ala Asp Val Ile Ser Asn Ala Ser
            100                 105
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<210> 35
<211> 204
<212> PRT
<213> Myrothecium

<220>
<221> MISC_FEATURE
<223> partial GPD protein sequence from the strain MUCL39210

<400> 35

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Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Ile Val Phe Arg Asn Ala
1               5                  10                  15
Val Glu His Pro Asp Ile Glu Ile Val Ala Val Asn Asp Pro Phe Ile
            20                  25                  30
Glu Thr Lys Tyr Ala Ala Tyr Met Leu Lys Tyr Asp Ser Thr His Gly
        35                  40                  45
Leu Phe Lys Gly Glu Val Glu Ala Asp Gly Ala Asp Leu Ser Val Asn
    50                  55                  60
Gly Lys Lys Val Arg Phe Tyr Thr Glu Arg Asp Pro Ala Ser Ile Pro
65                  70                  75                  80
Trp Lys Glu Thr Gly Ala Glu Tyr Ile Val Glu Ser Thr Gly Val Phe
                85                  90                  95
Thr Thr Thr Asp Lys Ala Lys Ala His Leu Ala Gly Gly Ala Lys Lys
            100                 105                 110
Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met Tyr Val Met Gly
        115                 120                 125
Val Asn Glu Lys Thr Tyr Asp Gly Ser Ala Asp Val Ile Ser Asn Ala
    130                 135                 140
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Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Leu Asn Asp
145 150 155 160
Lys Tyr Thr Ile Ile Glu Gly Leu Met Thr Thr Val His Ser Tyr Thr
165 170 175
Ala Thr Gln Lys Thr Val Asp Gly Pro Ser Ala Lys Asp Trp Arg Gly
180 185 190
Gly Arg Gly Ala Ala Gln Asn Ile Ile Pro Thr Thr
195 200

<210> 36
<211> 204
<212> PRT
<213> Myrothecium

<220>
<221> MISC_FEATURE
<223> partial GPD protein sequence from the strain MUCL11831

<400> 36

Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Ile Val Phe Arg Asn Ala
1 5 10 15
Val Glu His Asp Asp Val Glu Ile Val Ala Val Asn Asp Pro Phe Ile
20 25 30
Glu Pro Lys Tyr Ala Ala Tyr Met Leu Lys Tyr Asp Ser Thr His Gly
35 40 45
Leu Phe Lys Gly Glu Val Ser Val Asp Gly Ala Asp Leu Thr Val Asn
50 55 60
Gly Lys Lys Val Arg Phe Tyr Thr Glu Arg Asp Pro Ala Ala Ile Pro
65 70 75 80
Trp Lys Glu Thr Gly Ala Glu Tyr Ile Val Glu Ser Thr Gly Val Phe
85 90 95
Thr Thr Lys Asp Lys Ala Ala Ala His Leu Lys Gly Gly Ala Lys Lys
100 105 110
Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met Tyr Val Met Gly
115 120 125
Val Asn Glu Glu Thr Tyr Asp Gly Ser Ala Asp Val Ile Ser Asn Ala
130 135 140
Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile His Asp
145 150 155 160
Lys Phe Thr Ile Ile Glu Gly Leu Met Thr Thr Val His Ser Thr Leu
165 170 175
Pro Pro Arg Arg Pro Leu Thr Val Pro Pro Pro Arg Thr Gly Ala Val
180 185 190
Ala Val Val Leu Pro Arg Thr Ser Ser Pro Ala Ala
195 200

<210> 37
<211> 204
<212> PRT
<213> Myrothecium

<220>
<221> MISC_FEATURE
<223> partial GPD protein sequence from the strain CBS449.71

<400> 37

Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Ile Val Phe Arg Asn Ala
1 5 10 15
Val Glu His Ser Asp Val Glu Ile Val Ala Val Asn Asp Pro Phe Ile
20 25 30
Glu Pro Thr Tyr Ala Ala Tyr Met Leu Lys Tyr Asp Ser Thr His Gly

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        35                  40                  45
Val Phe Lys Gly Glu Val Thr Val Asp Gly Ala Asp Leu Thr Val Asn
    50                  55                  60
Gly Lys Lys Val Arg Phe Tyr Thr Glu Arg Asp Pro Ala Ala Ile Pro
65                  70                  75                  80
Trp Lys Glu Thr Gly Ala Asp Tyr Ile Val Glu Ser Thr Gly Val Phe
                85                  90                  95
Thr Thr Lys Asp Lys Ala Ala Ala His Leu Lys Gly Gly Ala Lys Lys
            100                 105                 110
Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met Tyr Val Met Gly
        115                 120                 125
Val Asn Glu Glu Thr Tyr Asp Gly Ser Ala Asp Val Ile Ser Asn Ala
    130                 135                 140
Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile His Asp
145                 150                 155                 160
Lys Phe Thr Ile Ile Glu Gly Leu Met Thr Thr Val His Ser Tyr Thr
                165                 170                 175
Ala Thr Gln Lys Thr Val Asp Gly Pro Ser Ala Lys Asp Trp Arg Gly
            180                 185                 190
Gly Arg Gly Ala Ala Gln Asn Ile Ile Pro Ser Thr
        195                 200
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